

(SEQ ID NO:3) represents the proposed head-to-tail structure of intact ITR arrays with alignment of sequence derived from individual clones. The junction of the inverted ITRs is marked by inverted arrowheads (at 251bp). Several consistent bp changes (shaded) were noted in the 5' ITR D-sequence (boxed) within four clones (p79, p81, p87, and p88). All bp changes are indicated in lower case letters.

Please amend the paragraph beginning at line 1, page 16 of the specification as follows:

Figure 11. Chemical sequence homology of three AAV circular intermediates (SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6) with various conformations of ITR arrays. Diversity in ITR arrays are evident from the non-conserved bases marked in lower case. The ends of the sequence (underlined) represent SphI restriction enzyme sites within head-to-tail circular AAV genomes cloned with the AV.GFP3ori shuttle virus.

Remarks

This Preliminary Amendment and the above-referenced SEQUENCE LISTING are being filed to conform the above-referenced application to the requirements of 37 C.F.R. §§ 1.821 - 1.825. In accordance with 37 C.F.R. § 1.821(e), a copy of the above-submitted SEQUENCE LISTING in ASCII computer readable form is submitted on even date herewith to the U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington VA 22202. It is respectfully submitted that the contents of the paper version of the SEQUENCE LISTING and the computer readable form being submitted to Box Sequence are the same. It is further submitted that the paper copy of the SEQUENCE LISTING and the computer readable form of the SEQUENCE LISTING do not represent new matter.